



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

<i>In re</i> Application of:)	
)	Group Art Unit: 1645
ZHELNIN and BLOOMQUIST)	
)	Examiner: S. Gucker
Serial No. 09/899,532)	
)	
Filing Date: July 6, 2001)	Docket No. 02973.00040

For: **HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR**

DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office
220 20th Street S.
Customer Window, Mail Stop AF
Crystal Plaza Two, Lobby, Room 1B03
Arlington, VA 22202

Dear Sir:

We, Leonid Zhelnin and Brian Bloomquist, declare as follows:

1. We are the named inventors of the subject matter claimed in the application referenced above.
2. Prior to March 2, 2000, we reduced to practice the subject matter of claims 1-8 and 12 of the application referenced above. The dates on the attached exhibits have been redacted; however, all the work described in this declaration was performed in the United States prior to March 2, 2000.
3. Prior to March 2, 2000, we searched for sequences that could be used to clone novel GPCRs with homology to orexin-2 and NPY1 receptors. We identified these sequences by

monitoring search results from a program (Gene Agent) that automatically checks sequences released into the public domain for homology to the orexin-2 and NPY1 receptors.

4. Prior to March 2, 2000, we received reports from both the Gene Agent program orexin-2 and NPY1 receptor searches indicating that DNAs within accession numbers EM:AC005961.1 (Homo sapiens Chromosome 11q12.2 PAC pDJ32L16 genomic DNA) and GB:g3823006 (Human sperm genomic library; Accession number AQ270411) each had homology to orexin-2 and NPY1 receptor sequences. Copies of the reports are attached as Exhibits 1 and 2.

5. Exhibit 1 identifies G3823006 as having homology to the orexin-2 receptor sequence. Pages 1 through 3 of Exhibit 1 contain analysis results from the search for sequences with homology to the orexin-2 receptor. See the top of page 1, which describes the "Project Name" as "orexin receptor homology search." In the "Protein Agent" box near the bottom of page 1, the location of G3823006 ("GB:g3823006") relative to the orexin-2 receptor sequence (OX2R) is shown. Pages 2 and 3 of Exhibit 1 contain initial information about G3823006 (beginning with the last set of boxes on page 2). Pages 4 and 5 of Exhibit 1 provide more detailed information on G3823006, including its length of 483 nucleotides.

6. Exhibit 2 identifies AC005961 as having homology to the orexin-2 receptor sequence. Pages 1 and 2 of Exhibit 2 also contain analysis results from the search for sequences with homology to the orexin-2 receptor. See the top of page 1, which describes the "Project Name" as "orexin receptor homology search." Page 2 of Exhibit 2 specifically contains information about AC005961 (last set of boxes on page 2). Page 3 of Exhibit 2 contains a summary of the search results for sequences with homology to the orexin-2 receptor. See the top of page 3, which indicates that the "Project Name" is "orexin receptor homology search." The

middle portion of page 3 (“Sequences”) contains a short description of each of the seven sequences identified by the search. These sequences include both accession numbers EM:AC005961 and GB:g3823006. Page 4 of Exhibit 1 provides additional information about accession number AC005961.1, including its length of 154,647 nucleotides.

7. We analyzed the sequences of these DNAs and found them to be overlapping. We selected the DNA sequence of Accession Number AC005961 to continue our efforts to obtain the sequence of our novel orexin- or NPY-like receptor (hereafter referred to as the “novel GPCR”).

8. BLAST analysis revealed that within AC005961 there were sequences comprising at least five exons with homology to the orexin-2 receptor. Exhibit 3 provides a copy of BLAST comparisons of five potential exons of an amino acid sequence of a putative novel GPCR encoded within Accession Number AC005961 (Sbjct) relative to the human orexin-2 receptor (Query) at page 1. Pages 2-3 of Exhibit 3 contain the description of the human orexin-2 receptor query sequence as found under Accession Number NP_001517.

9. Prior to March 2, 2000, we used sequence information from AC005961 to begin cloning the novel GPCR. We designed primers to amplify a portion of the novel GPCR from human genomic DNA using the polymerase chain reaction (PCR). We obtained PCR products of 161 bp (“NSAN.seq” or “GA1”) and 234 bp (“GA2”) from amplification of the genomic DNA. The 161 bp amplicon included DNA from transmembrane domains (TM) 1 and 2 of the putative novel GPCR. The 234 bp product included sequence from TM 3 and 4 domains of the putative novel GPCR.

10. A copy of the nucleotide sequences of the two PCR products is attached as Exhibit 4. Page 1 of Exhibit 4 describes the 161 bp sequence, which is identified by the

Sequence ID "NSAN.seq", as the "pcr of g3823006 GA1." Page 2 of Exhibit 4 shows the sequence of "NSAN.seq." Nucleotides 11-153 of the 161 base pair "NSAN.seq" amplification product are identical to nucleotides 167-309 of claimed SEQ ID NO: 1. Exhibit 5 provides an alignment of the "NSAN.seq" sequence with SEQ ID NO: 1. The first 10 and last 8 nucleotides of the 161 bp clone, which do not align with SEQ ID NO: 1, are not exonic sequence.

11. A description of the 234 bp amplification product, identified as "GA2" (see the Sequence ID), is provided on page 3 of Exhibit 4. Page 4 of Exhibit 4 provides the sequence of "GA2." Nucleotides 29-191 of the sequence of the "GA2" are identical to nucleotides 340-502 of claimed SEQ ID NO: 1. See Exhibit 6 for an alignment of "GA2 with SEQ ID NO: 1. The first 28 and last 43 nucleotides of the 234 bp clone do not align and presumably represent intronic sequence.

12. We designed primers to the 5'- and 3'-regions of the 161 bp amplification product, and performed 5'- and 3'-RACE to begin our effort to obtain the full-length nucleotide sequence of the novel GPCR. The reverse primers used in the strategy to extend the 5'-sequence of the novel GPCR were termed "GA1-85B" and "GA1-126B." These primers are shown on pages 2 and 3 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of Leonid Zhelnin's laboratory notebook pages 2 and 3 are provided as Exhibit 7.

13. The sequence of the "GA1-85B" primer is shown on the right side at the top of page 2 of Leonid Zhelnin's laboratory notebook. The sequence of the "GA1-126B" primer is shown on the right side at the top of page 2, beneath the sequence of the "GA1-85B" primer. Page 2 also shows the location of primers "GA1-85B" and "GA1-126B" on the 161 nucleotide sequence of "NSAN.seq". The sequence of each primer on the 161 nucleotide sequence is

circled, and “GA1-85B” and “GA1-126B” is handwritten above the location of each primer on the sequence.

14. Page 3 of Leonid Zhelnin’s laboratory notebook shows the location of the primers “GA1-85B” and “GA1-126B” on an alignment of the 161 bp subregion of G3823006, “NSAN.seq” (“GA1”). The sequence of each primer on the 161 nucleotide sequence is circled, and “GA1-85B” and “GA1-126B” is handwritten below the location of each primer on the sequence. The locations of nested PCR primers are also indicated.

15. Exhibit 8 shows the location of the “GA1-85B” and “GA1-126B” RACE primers against SEQ ID NO:1. The shaded box indicates the position of the 161 bp fragment, NSAN.seq; the identities of amino acids of the codons represented within the primers are included for reference purposes.

16. Prior to March 2, 2000, using the “GA1-85B” and “GA1-126B” primers, we obtained two 5'-RACE clones (210 and 347 bp) from human heart cDNA that were used to extend the sequence further 5' to NSAN.seq (GA1). Assembly of sequence data from the 5'-RACE clones and the 161 bp clone, NSAN.seq, revealed a 347 bp long ORF, named 5GA1. The predicted 103 amino-acid peptide encoded by this ORF had significant homology to the N-terminal regions of the NPY-1 and orexin-2 receptors.

17. The sequence of the nucleotide and encoded polypeptide of the 347 bp ORF, 5GA1, are provided in Exhibit 9, which contains a copy of pages 47 and 48 of Leonid Zhelnin’s laboratory notebook no. RB53651. Page 47 (page 1 of Exhibit 9), shows the nucleotide and encoded polypeptide sequence of the 347 bp RACE clone (top), and a ClustalW-formatted alignment of the predicted amino acid sequence of 5GA1 with the amino acid sequence of the neuropeptide Y1 receptor (NPY-1R.pep) (bottom). Page 48 (page 2 of Exhibit 9) shows a

ClustalW-formatted alignment of the predicted amino acid sequence of 5GA1 with the amino acid sequence of the orexin-2 receptor (Orexin 2.pep).

18. An alignment of the amino acid sequence encoded by 5GA1 with SEQ ID NO: 2 is provided in Exhibit 10. The alignment indicates that the amino acid sequence encoded by 5GA1 is identical to amino acid residues 1-103 of SEQ ID NO: 2. The last two predicted residues of 5GA1 are not represented in SEQ ID NO: 2.

19. An alignment of the nucleotide sequence of 5GA1 to SEQ ID NO: 1 is provided in Exhibit 11. The alignment shows that the nucleotide sequence of the 5GA1 clone is identical to nucleotides 1 – 309 of SEQ ID NO: 1. The nucleotide sequence of 5GA1 further extended the 161 bp sequence of NSAN.seq, the initial PCR fragment identical to nucleotides 167-309 of SEQ ID NO: 1 (see paragraph 6 and alignment in Exhibit 5), to include nucleotides 1 – 166 of SEQ ID NO: 1.

20. The position of the putative START methionine codon (ATG) in clone 5GA1 was consistent with clone 5GA1 being similar to the NPY-1 and orexin-2 receptors. The identity of this ATG as the true START codon was, however, unconfirmed at this point in the cloning because the open reading frame (ORF) was not closed upstream of the 5'-most ATG.

21. Documentation of the initial efforts to perform 3'-RACE are provided as Exhibit 12, which contains copies of pages 4 and 5 of Leonid Zhelnin's laboratory notebook no. RB53651. These pages show the location of the "forward" primers termed "GA1-F32" and "GA1-F41." The nucleotide sequence of primer "GA1-F32" is shown at the bottom of page 4 of Leonid Zhelnin's laboratory notebook. The nucleotide sequence of primer "GA1-F41" is shown as the nucleotide sequence immediately above the nucleotide sequence of primer "GA1-F32."

22. Page 4 of Leonid Zhelnin's laboratory notebook, the first page of Exhibit 12, also shows the location of each of primers "GA1-F32" and "GA1-F41" in the sequence of the 161 nucleotide clone ("NSAN.seq" or "GA1"). The nucleotide sequence of each primer is circled on "NSAN.seq." "GA1F41" is also handwritten above its nucleotide sequence in "NSAN.seq." "6AF32" is handwritten to the side of the nucleotide sequence for "GA1-F32". Exhibit 8, described above in paragraph 15, also diagrams the location of the forward primers relative to SEQ ID NO: 1.

23. The amplification conditions for performing 3'-RACE are provided on page 5 of Leonid Zhelnin's laboratory notebook, which is page 2 of Exhibit 12. The product of 3'-RACE can be seen in a photograph of an agarose gel provided at the bottom right-hand corner of page 1 of Exhibit 12, see particularly lanes 3 and 4 from the left.

24. We analyzed the sequence of the 3'-RACE amplicon procedure, which revealed that this clone contained sequences homologous to a GPCR through the seventh transmembrane domain, and ended in a polyadenosine stretch but with no STOP codon. Exhibit 13 is an alignment of two independent 3'-RACE amplicons, LZLZ11 and LZLZ21, with the "5GA1" consensus sequence as recorded on page 53 of Leonid Zhelnin's laboratory notebook no. RB53651.

25. LZLZ11 and LZLZ21 are 650 bp and 730 bp in length, respectively. When these two amplicons of overlapping sequence (see Exhibit 13, described in paragraph 24 above) are linked through PCR amplification they yielded a clone (3'-RACE #2). The 3'-RACE #2 clone is 913 bp in length. An alignment of 3'-RACE #2 clone with SEQ ID NO: 1 is shown in Exhibit 14A: The 913 base pair sequence of the 3'-RACE #2 clone is identical to nucleotides 230-1017 of SEQ ID NO: 1. An alignment of the amino acid sequence encoded by 3'-RACE #2 with SEQ

ID NO: 2 is shown in Exhibit 14B. The amino acid sequence encoded by 3'-RACE #2 is identical to amino acid residues 78-339 of SEQ ID NO: 2.

26. Assembling, by computer, the sequence of 3'-RACE #2 clone and clone 5GA1, we predicated a hypothetical 1036-nucleotide sequence encoding 345 amino acids. The sequence of the "virtual" 1036-nucleotide clone is identical to nucleotides 1-1017 of SEQ ID NO: 1. An alignment of these sequences is shown in Exhibit 15. The nucleotide sequences of the individual LZLZ11, LZLZ21 and 5GA1 sequences, which comprise the 3'-RACE #2 clone, are separately highlighted in Exhibit 15, pages 1 and 2.

27. The apparent poly(A) tail of the 3'-RACE #2 clone is not found in SEQ ID NO: 1. The 345 amino acid sequence encoded by the virtual clone is identical to amino acid residues 1-339 of SEQ ID NO: 2. An alignment of the 345-amino acid sequence with SEQ ID NO: 2 is provided on page 3 of Exhibit 15. Given the fact that the 3'-RACE #2 clone (and, hence, the virtual clone) had no STOP codon and an abnormally short C-terminal intracellular domain, we predicted that we still needed to identify more 3' sequence to complete the clone. The potential STOP codon highlighted at the bottom right of page 53 of Leonid Zhelnin's notebook no. RB53651 (Exhibit 13) actually is part of the Marathon-Ready™ cDNA adaptor in the vector.

28. Prior to March 2, 2000, we used the virtual sequence shown in Exhibit 13 as a template to search the Image Consortium database for novel expressed sequence tags (ESTs) to identify the missing 3'-nucleotide sequence. We identified three Image clones (named Im: 2055532, Im: 2055185, and Im: 2091776) from human kidney which had similarity to the virtual clone. Identification of the three Image clones was recorded at the top of page 61 of Leonid Zhelnin's laboratory notebook no. RB53651 (Exhibit 16).

29. Sequence analysis of Image clone 2055185 confirmed the putative START methionine described in paragraph 20 because it revealed an in-frame STOP codon upstream of this START methionine. Page 89 of Leonid Zhelnin's laboratory notebook no. RB53651 shows the START and STOP codons of the assembled sequence (Exhibit 17). The in-frame "TAG" STOP codon is boxed and begins 111 bp upstream of the first nucleotide of the START methionine, which is marked with an "M" at nucleotide 394 of the sequence.

30. We again performed a BLAST search of the sequence contained in AC005961 (as described in paragraph 4 above) to obtain the 3'-most sequence of the novel GPCR. We used a short stretch of sequence as query (about twenty nucleotides). The query sequence was located between the site of a several hundred-nucleotide unspliced intron and a stretch of 8 adenosine residues found in the sequence near the 3'-end of one of the Image clones. The top portion of Exhibit 18 diagrams the BLAST search strategy. Done this way, it was hoped that the search algorithm would not miss critical homologies with this short region which might otherwise be lost because of relevant sequence being "diluted" within a larger query sequence potentially broken up by other unidentified unspliced introns.

31. BLAST analysis identified the 279 nucleotide region that contained the putatively complete 3'-end and STOP codon of the novel GPCR. This information is provided as nucleotides 1411-1689 of the sequence on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651 (Exhibit 19 is a copy of page 89 of Leonid Zhelnin's laboratory notebook, the full-length sequence is referred to as LGZ1.seq).

32. The 279 nucleotides are identical to nucleotides 1018-1296 of SEQ ID NO: 1. An alignment of the 3'-most 300 nucleotides (279 bp of coding and 21 bp of 3'-untranslated) of the full-length novel GPCR, LGZ1, with SEQ ID NO:1 is provided in Exhibit 20.

33. The coding region of the novel GPCR included 1,296 nucleotides separated into 6 exons within the 154,647 nucleotides of genomic sequence AC005961. Exhibit 18, bottom diagram, shows the genomic structure of the novel GPCR.

34. Prior to March 2, 2000, we amplified clones containing the complete 1296-bp ORF as well as 5'- and 3'-untranslated DNA from both human heart and brain cDNA by PCR (using Marathon-Ready cDNA libraries, Clontech). The complete sequence of the novel GPCR was recorded on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. Exhibit 17, also described in paragraph 29, provides a copy of page 89 of Leonid Zhelnin's laboratory notebook. The 1296-bp ORF is identical to SEQ ID NO:1.

35. Also prior to March 2, 2000, we confirmed the coding sequence of the full-length cDNA clone by sequence analysis of a full-length amplicon generated by PCR from human brain cDNA. This sequence was recorded on pages 92 and 96-97 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of these pages are provided as Exhibit 21.

36. The coding sequence obtained by the sequence analysis is contained within SEQ ID NO:1 of our provisional application Serial No. 60/216,523, which is identical to SEQ ID NO:1 of our utility application 09/899,532. Exhibit 22 shows the 100% identity between SEQ ID NO: 1 and nucleotides 19 – 1335 of the sequence shown in Exhibit 21.

37. The amino acid sequence encoded by nucleotides 19 – 1335 in Exhibit 21 is identical to SEQ ID NO: 2 of our provisional application Serial No. 60/216,523, which is identical to SEQ ID NO: 2 of our utility application 09/899,523. An alignment of SEQ ID NO: 2 of the provisional and utility applications with the amino acid sequence shown in Exhibit 21 is provided in Exhibit 23. In addition, an alignment of the amino acid sequence shown in Exhibit 21 showing the constructs used to assemble SEQ ID NO: 2 is shown in Exhibit 24.

38. All statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: January 31, 2005

Brian T. Bloomquist
Brian T. Bloomquist, Ph.D.

Dated: January 31, 2005

Leonid Zhelnin
Leonid Zhelnin

Exhibit 1

Identification of G3823006



Analysis Results

[Main Menu](#) [Projects](#) [Query](#) [Seq Analysis](#) [Utilities](#) [Login / Logout](#) [Help](#)

Project ID: orexin Project Name: orexin receptor homology search
Created: Created By: Zheltnin, Leonid
Modified: Modified By: lt_Account, Admin
Status: OPEN Current User: Zheltnin, Leonid (WRITE)
Today's Date: Num Seqs: 7

Analysis Date:

These results are *saved*. Use the buttons to change the state of these results.

[Save These Results](#) [Discard These Results](#)

Description:

Maximum Number of Hits per Hit Class

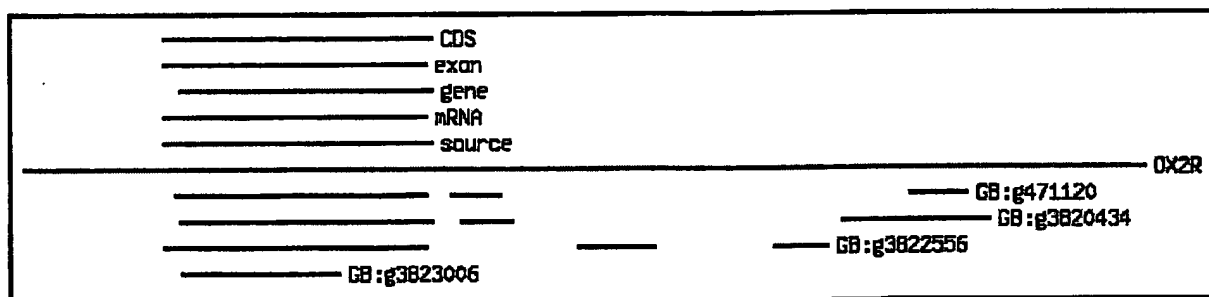
Trans. Protein:

Feature roll-up: ☐ Off ☒ On

[Redisplay](#)

[View parameters](#)

Protein Agent



☐ orexin:OX2R:1

Hit ID	P-Value	% ident.	Description	Hit Class
<input checked="" type="checkbox"/> <u>GB:g471120:2</u>	8.8e-19	34	Human mRNA for angiotensin II type 1b receptor, complete cds.	Trans. Protein
Result Details	Feature	Description	Feature Metric	Value

	CDS					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	61	160	+			
	source					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	61	160	+			
Hit ID	P-Value	% ident.	Description			Hit Class
<input checked="" type="checkbox"/> GB:q3820434:2 Result Details	2.2e-18	30	Mus musculus mRNA for G-protein coupled receptor, complete CDS.			Trans. Protein
	Feature	Description			Feature Metric	Value
	CDS					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	62	162	+			
	gene					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	62	162	+			
	source					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	62	162	+			
Hit ID	P-Value	% ident.	Description			Hit Class
<input checked="" type="checkbox"/> GB:q3822556:1 Result Details	3.6e-14	33	Bos taurus oxytocin receptor gene, promoter region and partial cds.			Trans. Protein
	Feature	Description			Feature Metric	Value
	CDS					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	56	160	+			
	exon					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	56	160	+			
	mRNA					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	56	160	+			
	source					
	Left End	Right End	Strand	Component Description	Component Metric	Value
	56	160	+			
Hit ID	P-Value	% ident.	Description			Hit Class
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	Feature	Description			Feature Metric	Value

	source							
		Left End	Right End	Strand	Component Description	Component Metric	Value	
		63	125	+				

Select All Deselect All

Save to Project Submit Reset

Requested by: Zhelnin, Leonid





Query Detail

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
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Sequence: GB:g3823006:1



Entries with the same Physical Sequence Newgag:g3823006:1 orexin:g3823006:1		FASTA	
General Information About The Entry			
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Version	1		
Sequence Description	HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.		
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Database Description	Nucleotide and Protein Sequence Data Bank		
Molecule	DNA		
Database Division	GSS		
Entry Header Line	AQ270411 483 bp DNA GSS		
Alternate Keys	LOCUS AQ270411 PRIMARY AC AQ270411		
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Sequence Header Line	155 a 84 c 169 g 73 t 2 others		
Origin and Alternate Names			
Keywords	GSS		
Organism	Homo sapiens		
Taxonomy	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Species	HOMO SAPIENS		
Biological Tissue Source	human.		
Comments			
<ul style="list-style-type: none">•• Contact: Mahairas GG, Wallace JC, Hood L• High Throughput Sequencing Center• University of Washington• 401 Queen Anne Avenue North, Seattle, WA 98109, USA• Tel: (206) 616-3618• Fax: (206) 616-3887• Email: jwallace@u.washington.edu• Sequence Tagged Connector• Plate: 2052 row: N column: 7• Class: BAC ends			

- High quality sequence stop: 483.

References

[1]	(bases 1 to 483)
Title	Construction of a Characterized Clone Resource for Genomic Sequencing
Journal	Unpublished
Authors	Mahairas G.G. Wallace J.C. Smith K. Swartzell S. Furlong J. Shaker R. Schmidt S. Traicoff R. Hood L.E.

Hits and FeaturesPublic Source**Public Source****Feature 1**

source

1..483

1 .. 483 (+ strand)

Feature Qualifiers

clone Plate=2052 Col=7 Row=N

clone_lib CIT Approved Human Genomic Sperm Library D

organism Homo sapiens

sex male

Feature Cross Referencestaxon 9606**Feature Notes**Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B**INCYTE PHARMACEUTICALS, INC.**

Exhibit 2

Identification of AC005961



Analysis Results

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
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Project ID: orexin Project Name: orexin receptor homology search
 Created: Created By: Zhelnnin, Leonid
 Modified: Modified By: lt_Account, Admin
 Status: Current User: Zhelnnin, Leonid (WRITE)
 Today's Date: Num Seqs: 7

Analysis Date:

These results are *saved*. Use the buttons to change the state of these results.

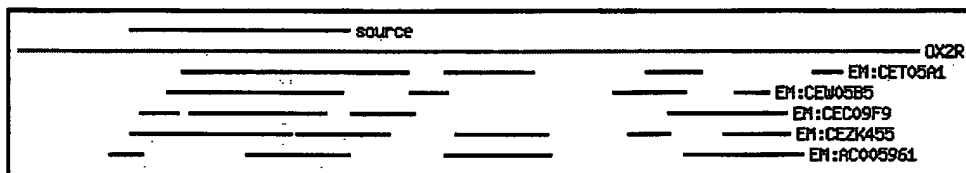
Description:

Maximum Number of Hits per Hit Class

Trans. Protein:
 Feature roll-up: ☐ Off ☒ On

[View parameters](#)

Protein Agent



☐ orexin:OX2R:1

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	Feature	Description				Feature Metric	Value
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Hit ID	P-Value	% ident.	Description				Hit Class
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	Feature	Description				Feature Metric	Value
		source					
		Left End	Right End	Strand	Component Description	Component Metric	Value

		74	133	+			
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	Feature	Description				Feature Metric	Value
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	Left End	Right End	Strand	Component Description	Component Metric	Value	
	85	152	+				
Hit ID	P-Value	% ident.	Description				Hit Class
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	Feature	Description				Feature Metric	Value
	source						
	Left End	Right End	Strand	Component Description	Component Metric	Value	
	56	134	+				
Hit ID	P-Value	% ident.	Description				Hit Class
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	Feature	Description				Feature Metric	Value
	source						
	Left End	Right End	Strand	Component Description	Component Metric	Value	
	112	163	+				

Requested by: Zhelnin, Leonid



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Project Summary

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Project ID: orexinProject Name: orexin receptor homology search

Created:

Created By: Zhelnin, Leonid

Modified:

Modified By: lt_Account, AdminStatus: OPENCurrent User: Zhelnin, Leonid (WRITE)

Today's Date:

Num Seqs: 7
[Project Members](#)
[Project Status](#)
[Analysis Tools](#)
[Create Agent](#)

Sequences (7 of 7 shown, 7 Active):

Sequence ID	Type	Parent	Created By	Created	Status
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HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.					
<u>orexin:AC005961:1</u>	DNA	<u>EM:AC005961</u>	Zhelnin, L.		OPEN
*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.					
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<u>orexin:G2897124:1</u>	PRT	<u>ST:G2897124</u>	Zhelnin, L.		OPEN
OREXIN RECEPTOR-1.					
<u>orexin:OX2R:1</u>	PRT		Zhelnin, L.		OPEN
P1;G2897128 - orexin receptor-2 - Homo sapiens (human)					
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Homo sapiens orexin receptor-1 mRNA, complete cds.					

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Gene Agent Results (10 of 166 shown, 166 active):

Agent Name	Results	Started On	Description	Status	Method	Job Status
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<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed

[List All Gene Agent Results](#)



Query Detail

Main Menu	Projects	Query	Seq Analysis	Utilities	Login / Logout	Help
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Sequence: orexin:AC005961:1 [Add Sequence Annotation](#)



Entries with the same Physical Sequence <u>Imagelga:q3859648:1</u> <u>Newqage:AC005961:1</u>		<u>FASTA</u>
General Information About The Entry		
Sequence ID	AC005961	
Version	1	
Sequence Description	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.	
Project	orexin	
Project Name	orexin receptor homology search	
Molecule	DNA	
Sequence Information		
Length	154647	

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Exhibit 3

Homology between
AC005961 and the orexin-2
receptor

		Reading Frame	High Score	Small Su Proba P(N)
Sequences producing High-scoring Segment Pairs:				
AC005961 *** SEQUENCING IN PROGRESS *** Homo sapien..		+2	103	1.8e-
Score = 103 (48.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 17/52 (32%), Positives = 33/52 (63%), Frame = (+2)				
Query: 112 LVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRWYAICHPLMFK	163			
L+ D++ G +CK++P++Q+ +V +LT++CIA++R + HP K				
Sbjct: 48452 LMYDLSYFLTAGAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMK	48607			
Score = 88 (41.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 15/54 (27%), Positives = 31/54 (57%), Frame = (+3)				
Query: 210 CDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ	263			
C E W ++ K+Y ++ ++ PL +M++ Y +I +LW ++ G SV++				
Sbjct: 56082 CLEEWTSVPVHQKIYTTFILVILFLLPLMVMLILYSKIGYELWIKKRVGDGSVLR	56243			
Score = 71 (33.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 15/54 (27%), Positives = 26/54 (48%), Frame = (+1)				
Query: 329 VFGMFAHTEDRETIVYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAFSCC	382			
+ G F D T+ F + ++NS NPI+Y F++ F++ +A C				
Sbjct: 59380 ISGNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIVYAFMNENFKKNVLSAVCYC	59541			
Score = 47 (22.1 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 9/17 (52%), Positives = 11/17 (64%), Frame = (+2)				
Query: 46 EYLHPKEYEWVLIAGYI	62			
EY H +E W LI+ YI				
Sbjct: 29786 EYPHAE*NTLISQYI	29836			
Score = 46 (21.6 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = (+3)				
Query: 381 CCCLGVHH	388			
CCCLG+ H				
Sbjct: 148296 CCCLGLEH	148319			

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD

☐ 1: [NP_001517](#). Reports orexin receptor 2...[gi:4557639] BLink, Domains, Links

LOCUS NP_001517 444 aa linear PRI
 DEFINITION orexin receptor 2 [Homo sapiens].
 ACCESSION NP_001517
 VERSION NP_001517.1 GI:4557639
 DBSOURCE REFSEQ: accession NM_001526.2
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 444)
 AUTHORS Karteris,E., Chen,J. and Randeva,H.S.
 TITLE Expression of human prepro-orexin and signaling characteristics of
 orexin receptors in the male reproductive system
 JOURNAL J. Clin. Endocrinol. Metab. 89 (4), 1957-1962 (2004)
 PUBMED [15070969](#)
 REMARK GeneRIF: both OX1R and OX2R are expressed in the testis,
 epididymis, penis, and seminal vesicle
 REFERENCE 2 (residues 1 to 444)
 AUTHORS Peyron,C., Faraco,J., Rogers,W., Ripley,B., Overeem,S., Charnay,Y.,
 Nevsimalova,S., Aldrich,M., Reynolds,D., Albin,R., Li,R., Hungs,M.,
 Pedrazzoli,M., Padigaru,M., Kucherlapati,M., Fan,J., Maki,R.,
 Lammers,G.J., Bouras,C., Kucherlapati,R., Nishino,S. and Mignot,E.
 TITLE A mutation in a case of early onset narcolepsy and a generalized
 absence of hypocretin peptides in human narcoleptic brains
 JOURNAL Nat. Med. 6 (9), 991-997 (2000)
 PUBMED [10973318](#)
 REFERENCE 3 (residues 1 to 444)
 AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
 Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
 Wilson,S., Arch,J.R., Buckingham,R.E., Haynes,A.C., Carr,S.A.,
 Annan,R.S., McNulty,D.E., Liu,W.S., Terrett,J.A., Elshourbagy,N.A.,
 Bergsma,D.J. and Yanagisawa,M.
 TITLE Orexins and orexin receptors: a family of hypothalamic
 neuropeptides and G protein-coupled receptors that regulate feeding
 behavior
 JOURNAL Cell 92 (5), 1 (1998)
 PUBMED [9527442](#)
 REFERENCE 4 (residues 1 to 444)
 AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
 Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
 Wilson,S., Arch,J.R., Buckingham,R.E., Haynes,A.C., Carr,S.A.,
 Annan,R.S., McNulty,D.E., Liu,W.S., Terrett,J.A., Elshourbagy,N.A.,
 Bergsma,D.J. and Yanagisawa,M.
 TITLE Orexins and orexin receptors: a family of hypothalamic
 neuropeptides and G protein-coupled receptors that regulate feeding
 behavior
 JOURNAL Cell 92 (4), 573-585 (1998)
 PUBMED [9491897](#)
 REFERENCE 5 (residues 1 to 444)
 AUTHORS Flier,J.S. and Maratos-Flier,E.
 TITLE Obesity and the hypothalamus: novel peptides for new pathways
 JOURNAL Cell 92 (4), 437-440 (1998)
 PUBMED [9491885](#)
 REFERENCE 6 (residues 1 to 444)
 AUTHORS de Lecea,L., Kilduff,T.S., Peyron,C., Gao,X., Foye,P.E.,
 Danielson,P.E., Fukuhara,C., Battenberg,E.L., Gautvik,V.T.,

Bartlett, F.S. II, Frankel, W.N., van den Pol, A.N., Bloom, F.E.,
Gautvik, K.M. and Sutcliffe, J.G.
TITLE The hypocretins: hypothalamus-specific peptides with
neuroexcitatory activity
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (1), 322-327 (1998)
PUBMED [9419374](#)
COMMENT **REVIEWED REFSEQ:** This record has been curated by NCBI staff. The
reference sequence was derived from [AF041245.1](#).

Summary: HCRT2 is a G-protein coupled receptor expressed
exclusively in the brain. It has 64% identity with HCRT1. HCRT2
binds both orexin A and orexin B neuropeptides. HCRT2 is involved
in the central feedback mechanism that regulates feeding behaviour.

FEATURES Location/Qualifiers
source 1..444
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p11-q11"
Protein 1..444
/product="orexin receptor 2"
/note="orexin receptor-2; hypocretin receptor-2"
CDS 1..444
/gene="HCRT2"
/coded_by="NM_001526.2:325..1659"
/note="go_component: integral to plasma membrane [goid
0005887] [evidence TAS] [pmid 9491897];
go_function: orexin receptor activity [goid 0016499]
[evidence IEA];
go_function: rhodopsin-like receptor activity [goid
0001584] [evidence IEA];
go_function: neuropeptide receptor activity [goid 0008188]
[evidence TAS] [pmid 9491897];
go_process: feeding behavior [goid 0007631] [evidence TAS]
[pmid 9491897];
go_process: synaptic transmission [goid 0007268] [evidence
TAS] [pmid 9491897];
go_process: neuropeptide signaling pathway [goid 0007218]
[evidence TAS] [pmid 9491897]"
/db_xref="GeneID:3062"
/db_xref="LocusID:3062"
/db_xref="MIM:602393"

ORIGIN

```
1 msgtkledsp pcrnwssase lnetqepfln ptdydeefl rylwreylhp keyewvliag
61 yiiivfvvali gnlvvcvavw knhhmrtvtn yfivnlsiad vlvttitclpa tlvvditetw
121 ffgqslckvi pylqtvsvsv svltlscial drwyaichpl mfkstakrar nsiviiwivs
181 ciimipqaiw mecstvfpgl ankttlftvc derwggeiyp kmyhicfflv tymaplclmv
241 laylqifrk1 wcrqipgtss vvqrkwkplq pvsqprgpgq ptksrmsava aeikqirarr
301 ktarmmlmv1 lvfaicylpi silnvlkrvf gmfahtedre tvyawftfsh wlvyanasaan
361 piiynflsgk freefkaafs ccclgvhhrq edrltrgrts tesrkslttq isnfdniskl
421 seqvvltsis tlpaangagp lqnw
```

//

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Exhibit 4

Description of the 161 bp
fragment (NSAN.seq or
GA1) and 234 bp fragment
(GA2)



Query Detail

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Sequence: Newgage:NSAN.seq:1 [Add Sequence Annotation](#)

Entries with the same Physical Sequence		FASTA
General Information About The Entry		
Sequence ID	NSAN.seq	
Version	1	
Sequence Description	pcr of g3823006 GA1	
Project	Newgage	
Project Name	Cloning new gene agent search sequences	
Molecule	DNA	
Sequence Information		
Length	161	





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Project ID:	<u>Newgag</u>	Project Name:	Cloning new gene agent search sequences
Created:		Created By:	Zhelnin, Leonid
Modified:		Modified By:	Zhelnin, Leonid
Status:	OPEN	Current User:	Zhelnin, Leonid (WRITE)
Today's Date:		Num Seqs:	<u>30</u>

>Newgag:NSAN.seq:1 pcr of g3823006 GA1
AGTGTAATCATCGCCCTGGCGCTCTTTGGCAATGCTCTGGTGTCTACGTGGTGACCCGAGCAAGGCCATGCGCACCGT
CACCAACATCTTTATCTGCTCCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCATTCCCGTCACCATGAAGCCGA
A

Requested by: Zhelnin, Leonid



LifeTools
biology in silico**Query Detail**[Main Menu](#)[Projects](#)[Query](#)[Seq Analysis](#)[Utilities](#)[Login / Logout](#)[Help](#)Sequence: **Newgag:GA2:1** [Add Sequence Annotation](#)

Entries with the same Physical Sequence		<u>FASTA</u>
General Information About The Entry		
Sequence ID	GA2	
Version	1	
Sequence Description	pcr product of ac acl primers of AC00596 genomic chromosome seq in progress	
Project	Newgage	
Project Name	Cloning new gene agent search sequences	
Molecule	DNA	
Sequence Information		
Length	234	

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LifeTools™
biology in silico**Retrieve
FASTA Sequences**[Main Menu](#)[Projects](#)[Query](#)[Seq Analysis](#)[Utilities](#)[Login / Logout](#)[Help](#)

Project ID:	<u>Newgage</u>	Project Name:	Cloning new gene agent search sequences
Created:		Created By:	Zhelnin, Leonid
Modified:		Modified By:	Zhelnin, Leonid
Status:	OPEN	Current User:	Zhelnin, Leonid (WRITE)
Today's Date:		Num Seqs:	<u>30</u>

>**Newgage:GA2:1** pcr product of ac acl primers of AC00596 genomic chromosome se
GTATGATTTATCCTATTTCTTACTGCAGGTGCTTTTCATTTGCAAGATGGTGCCATTTGTCCAGTCTACCGCTGTTGTGA
CAGAAATCCTCACTATGACCTGCATTGCTGTGGAAAGGCACCAGGGACTTGTGCATCCTTTTAAAATGAAGTGGCAATAC
ACCAACCGAAGGGCTTTCACAATGCTAGGTGAGGCCACTGGATGTGCCAATGGCAGTGTGAATGACATTCTTCA

Requested by: Zhelnin, Leonid

**INCYTE PHARMACEUTICALS, INC.**

Exhibit 5

Nucleotide sequence
comparison of NSAN.seq to
SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75
 1 M Q A L N I T P E Q F S R L L R D H N L T R E Q F 25

76 ATC GCT CTG TAC CGG CTG CGA CGG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150
 26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50

AGTGACTCA

TC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 225
 151 ACC GGC GTG CTC ATC TTC GGC CTC GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 75
 51 T G V L I F A L A L F G N A L V F Y V T R S K A

TM1

ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300
 226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 100
 76 M R T V T N I F I C S L A L S D L L I T F F C I P

TM2

AAGCCGAA

GTC ACC ATG 375
 301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 125
 101 V T M L Q N I S D N W L G G A F I C K M V P F V Q

376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450
 126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150

TM3

451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525
 151 F K M K W Q Y T N R R A F T M L G V V W L V A V I 175

TM4

526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600
 176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTG 675
 201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225

TM5

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750
 226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
 251 S V L R T I H G K E M S K I A R K K R A V I M M 275

826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900
 276 V T V V A L F A V C W A P F H V V H M M I E Y S N 300

TM6

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975
 301 F E K E Y D D V T I K M I F A I V Q I I G F S N S 325

TM7

976 ATC TGT AAT CCC AAT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050
 326 I C N P I V Y A F M N E N F K K N V L S A V C Y C 350

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125
 351 I V N K T F S P A Q R H G N S G I T M M R K A K 375

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200
 376 F S L R E N P V E E T K G E A F S D G N I E V K L 400

1201 TGT GAA CAG ACA GAG AAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275
 401 C E Q T E E K K L K R H L A L F R S E L A E N S 425

1276 CCT TTA GAC AGT GGG CAT TAA
 426 P L D S G H *

1296
 431

Exhibit 6

Alignment of 234 bp
fragment to SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75
1 M Q A L N I T P E Q F S R L L R D H N L T R E Q F 25

76 ATC GCT CTG TAC CCG CTG CGA CCG CTG CAC ACC CCA GAG CTG CCG GGA CGG GGC AAC CTG GCC CTC GTG CTC 150
26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50

151 ACC GGC GTG CTC ATC TTC GCC CTG CCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG GTG ACC CGC AGC AAG GCC 225
51 T G V L I F A L A L F G N A L V F Y V T R S K A 75

TM1

226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300
76 M R T V T N I F I C S L A L S D L L I T F F C I P 100

TM2

GTATGATTTATCCTATTTCCTTACTGCA

301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375
101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125

TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450
376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 150
126 S T A V V T E I L T M T C I A V E R H Q G L V H P

TM3

AGGCCACTGGATGGCAATGGCAGTGTGAATGACATTCTTCA

TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT G 525
451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG CTC TGG CTG GCA GTC ATC 175
151 F K M K W Q Y T N R R A F T M L G V V W L V A V I

TM4

526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600
176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTC 675
201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225

TM5

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC ACT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750
226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
251 S V L R T I H G K E M S K I A R K K R A V I M M 275

Exhibit 7

RACE primers

BAYER CORPORATION

SUBJECT

5' RACE 6A1 - 1A

1	9	1	85	85	54.1	74.1	4.9	54.1	56.8	61.7	48.1	60.0	-0.3	7.9	
2	*														
3															
4	*	10	1	126	126	54.8	77.0	1.7	56.0	56.8	58.6	48.1	48.0	-8.3	-7.8
5															
6															
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30															
31															
32															
33															
34															

GA1.txt Translated Sequence

Sequence Range: 1 to 161

double strand probe

10 20 30 40 50
 (C)CCTCCTGTC ACCGG AGTGTACTCATCGCCCTGGCCCTCTTTGGCAATGCTCTGGTGTCTACGT
 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCACAAGATGCA
 S V L I A L A L F G N A L V F Y V
 TRANSLATION OF GA1.TXT [A]
 60 70 80 90 100
 GGTGACCCGCGAGCAAGGCCATGCGCACCGTCACCAACATCTTTATCTGCT
 CCACTGGGCGTCGTTCCGGTACGGTGGCAGTGGTTGTAGAAATAGACGA
 V T R S K A M R T V T N I F I C
 TRANSLATION OF GA1.TXT [A]
 110 120 130 140 150
 CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTCTGCAATCCCGTCACC
 GGAACCGCGAGTCACTEGACGAGTAGTGGAGAGACGTAAEGGCACTGG
 S L A L S D E F F E C I P V T
 TRANSLATION OF GA1.TXT [A]
 160
 ATGAAGCCGAA
 TAGTTCGGCTT
 M K P X

5 primers for 5' RACE

probe:

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES:

GB g3823006. by GA1.txt Aligned Sequence

Sequence Range: 1 to 481

GB g382300 AGCGCGCAAGATGACCTCGTGTCAACCGAGTGTA¹⁰TACTCATCGCCCTGGCGC²⁰
TCGCGCGTTCTACTGGAGCACAGTGGCCTCACATGA³⁰TGCTGCTGCTGC⁴⁰

```
    jmp1 str +
```

10 20
AGTGTA CT CATCGCCCTGGCGC

GB 9382300

AGTGTACTCATCGCCCTGGCGC
S V L I

GB g382300 TCTTAGGAGTGTGGTGTTTACAGTGGTGACCAGCAGCAAGACCATG
AGAATGCGTGAAGACACAAATGTCA CCACTGGTCGTCGTTCTGGTAC

```

      jmp1 str + TCTTTGGCAAGTGTGACCGCAGCAAGGCCATG>

```

GB g382300 TCTTAGCAAATGCTTTGGTGTTTACAGTGGTGACCAGCAGCAAGACCATG

GB g382300 CGCACCCTCACCAACATCTTATGTCCTCCTTGCGGTTCAGTGACTGCTC
GCTGGCAGTGGTTGTAGATAATAGACGAGGAACCGCTGCTGCTGCTG

jmp1 str + (bA) - N² CAGTGACCTGCTC>

GB g382300 6A1-1B TCAGTGA CTGCTC

```

      80          90          100          110          120
jmp1 str + CGCACCGTCACCAACATCTTTATCTGCTCCTTGGCGCTCAGTGACTGCT>

```

GB g382300 CGCACCGTCACCAACATCTATATCTGCTCCTTGGCGCTCAGTGACTGCTC

GB g382300 ATCACCTTCTTCTGCATTCCCCGTACCATGCTCCAGAACATTTCCGACAA
TAGTCCGGGACCTCGAAGCAGCACTGGGAGAGTGAGGTCTTGTAAGGCTGTT

```

      100      200      300      400
jmp1 str + ATCACCTTCTTCTGCATTCCCGTCACCATGAAGCCGAA

```

GB g382300 ATCACCTTCTTCTGCATTCCCGTCACCATGCTCCAGAA

MKP

CATC

'NOLDS / NILES. MI ' SEPT. 95

SIGNED BY**DATE**

WITNESSED AND UNDERSTOOD BY

DATE _____

Exhibit 8

Locations of RACE primers
on SEQ ID NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75

76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150

GA1-F41

(L F G N A L V F Y)
CTC TTT GGC AAT GCT CTG GTG TTC TAC

151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG ACC CGC AGC AAG GCC 225

CGA GAC CAC AAG ATG CAC CAC TGG G
(A L V F Y V T R)

GA1-85B

GA1-F32

(R T V T N I F I C)

GC ACC GTC ACC AAC ATC TTT ATC TG

226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC ACT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300

G TGG CAG TGG TTG TAG AAA TAG ACG
(R T V T N I F I C)

GA1-126B

301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375

376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450

451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525

526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC CTG 675

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825

826 GTG ACA GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900

901 TTT GAA AAG GAA TAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975

976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200

1201 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275

1276 CCT TTA GAC AGT GGG CAT TAA 1296

Exhibit 9

5GA1 vs. NPY1 and OX-2

BAYER CORPORATION

SUBJECT

GA1-5 RACE product

*** DNA Strider™ 1.2 ***

Untitled Sequence # 3 -> Genes

DNA sequence 347 b.p. CTTGCCCGCCG ... CATGAGCCGAA linear

[illegible]

5GA1 Aligned Sequences Formatted Alignments

ClustalW Formatted Alignments

5GA1
NPY-1R.pep

5GA1 L R P L V Y T P E **P** G R A K L **A** V **T** G V L **I** F A **A** **E**
 NPY-1R.pep D - - - - D C H **D** L A M I F **T** **A** **A** Y G A V **I** **I** **G** V

5GA1
NPY-1R.pep

F A L V F Y V T R S K A N P T V I L F C S L A L

S G L A I I I L L K O E M R N N L L V N S F

70 80 90

5GA1
NPY-1R.pep

100 110 120

D I L T F F C I V M K P
D L V A I M C L F F V Y T L M D H W V F G E A M C K L

SIGNED BY

DATE _____

WITNESSED AND UNDERSTOOD BY

DATE _____

BAYER CORPORATION

SUBJECT

SA-RACE

Orexin 2.pep Aligned Sequences Formatted Alignments

ClustalW Formatted Alignments

```

Orexin 2.pep      10      20      30
5GA1      S G T K L E D S P C R N W S S A S E L N E I O P E L N
           Q A L N I T - - - E Q F S R L L R D H N L E R E Q Q L A

Orexin 2.pep      40      50      60
5GA1      P T D Y D D E E F R Y W R E Y L H K E Y E W V F A G
           L Y R - - - - - L R P V Y T P E L G R A K L A Y L T

Orexin 2.pep      70      80      90
5GA1      Y I I V V V V I C N V C V A W K N H A M R T V I N
           G V L I A L A L F S A I V F Y V T S K A M R T V I N

Orexin 2.pep      100     110     120
5GA1      Y V N I S L A I V V I T L P A I L V V D I T E T W
           I C S L A I S D L L I F F C L P V M K P
    
```

↑ 210 by 6 Hrs

gi14758820 neuropeptide G protein-coupled receptor gb|AAD22047.1|
(AF119815) G-protein-coupled receptor [Homo sapiens]
Length = 522

Score = 152 (73.0 bits), Expect = 1.8e-13, P = 1.8e-13
Identities = 27/55 (49%), Positives = 42/55 (76%)

Query: 49 VLTGVLIFALALPGNALVFYVTRSKAMRTVINIFCSLALSDLLITFFCIPVTM 103
+++ LIP L + GN +V ++V R+K M TVIN+FI +LA+SDLL+ FC+P+T+
Sbjct: 151 IISYPLIFFLCMAGNTVVCFFVMRNKGMHTVINLFIILNLAISDLLVGIFCMPITL 205

>>SP:NY2R_PIG NEUROPEPTIDE Y RECEPTOR TYPE 2 (NPY2-R). (383 aa)
initn: 123 initl: 123 opt: 181 Z-score: 234.1 expect(): 2.5e-06
Smith-Waterman score: 181; 45.100% identity in 71 aa overlap

```

          10      20      30      40      50      60
ga1      PEQFSRLLRDHNLTREQFIALYRLRPLVYTPPELPGRAKLA-----LVLGTGLIFALALPG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
SP:NY2R_PIG DENQTVVEEMKMEPSGPGHTTFRGELAPDSEPELKDKSTKLIEVQIILILAYCSIIILGVVG
          10      20      30      40      50      60
    
```

```

          70      80      90      100
ga1      NALVFYVTRSKAMRTVINIFCSLALSDLLITFFCIPVTM KP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
SP:NY2R_PIG NSLVHVVVKFKSMRTVINFFIANLAVADLLVNTLCPLPTLTITMGEMWKGPFVLCVLP
          70      80      90      100      110      120
    
```

```

SP:NY2R_PIG YAQGLAVQVSTITLTIVIALDRHRCIVYHLESKISKISRFSLIIGLAWGISALLASPLAIFR
          130      140      150      160      170      180
    
```

SIGNED BY

DATE

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DATE

CROSS REFERENCES:

Exhibit 10

Alignment of 5GA1 with
SEQ ID NO 2

1	M Q A L N I T P E Q F S R L L R D H N L T R E Q F
26	I A L Y R L R P L V Y T P E L P G R A K L A L V L
51	T G V L I F A L A L F G N A L V F Y V T R S K A
76	M R T V T N I F I C S L A L S D L L I T F F C I P
101	V T M L Q N I S D N W L G G A F I C K M V P F V Q
126	S T A V V T E I L T M T C I A V E R R H Q G L V H P
151	F K M K W Q Y T N R R A F T M L G V V L V A V I
176	V G S P M W H V Q Q L E I K Y D F L Y E K E H I C
201	C L E E W T S P V H Q K I Y T T F I L V I L F L L
226	P L M V M L I L Y S K I G Y E L W I K K R V G D G
251	S V L R T I H G K E M S K I A R K K R A V I M M
276	V V V A L F A V C W A P F H V V H M M I E Y S N
301	F E K E Y D D V T I K M I F A I V Q I I G F S N S
326	I C N P I V Y A F M N E N F K K N V L S A V C Y C
351	I V N K T F S P A Q R H G N S G I T M M R K K A K
376	F S L R E N P V E E T K G E A F S D G N I E V K L
401	C E Q T E E K K K L K R H L A L F R S E L A E N S
426	P L D S G H *

Exhibit 11

Alignment of 5GA1
nucleotide sequence with
SEQ ID NO 1

31 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 105
1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75
1 M Q A L N I T P E Q F S R L L R D H N L T R E Q F 25
106 ATC GCT CTG TAC CGG CTG CGA CGG CTG GTC TAC ACC CCA GAG CTG CGG GGA CGC GCC AAG CTG GCC CTC GTG CTC 180
76 ATC GCT CTG TAC CGG CTG CGA CGG CTG GTC TAC ACC CCA GAG CTG CGG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150
26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50
181 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC CTG GTG ACC CGC AGC AAG GCC 255
151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC CTG GTG ACC CGC AGC AAG GCC 225
51 T G V L I F A L A L A L F G N A L V F Y V V T R S K A 75
256 ATG GCG ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 330
226 ATG GCG ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300
76 M R T V T N I F I C S L A L S D L L I T F F C I P 100
331 GTC ACC ATGAGCCGAA 347
301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375
101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125
376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450
126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150
451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525
151 F K M K W Q Y T N R R A F T M L G V V W L V A V I 175
526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600
176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200
601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTG 675
201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225
676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750
226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250
751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
251 S V L R T I H G K E M S K I A R K K R A V I M M 275
826 GTG ACA GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT CAT ATG ATG ATT GAA TAC AGT AAT 900
276 V T V V A L F A V C W A P F H V V H M M I E Y S N 300

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975
 301 F E K E Y D D GAT GAT GTC ACA ATC AAG ATG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 325

 976 ATC TGT AAT CCC AAT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050
 326 I C N P I V Y A F M N E N F K K N V L S A V C Y C 350

 1051 ATA GTA AAT AAA ACC TTC TCT CCA CCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125
 351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375

 1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200
 376 F S L R E N P V E E T K G E A F S D G N I E V K L 400

 1201 TGT GAA CAG ACA GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275
 401 C E Q T E E K K L K R H L A L F R S E L A E N S 425

 1276 CCT TTA GAC AGT GGG CAT TAA 1296
 426 P L D S G H * 432

Exhibit 12

3' RACE primers

BAYER CORPORATION

3' RACE

SUBJECT

Translated Sequence

6A1 F41

New

Page 1

Range: 1 to 161

10 20 30 40 50
 AGTGACTCATCGCCCTGGCCCTTTTGGCAATGCTCTGGTGTCTACGT
 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCACAAGATGCA
 S V L I A L A L F G N A L V F Y V>

TRANSLATION OF GA1.TXT [A]

nexted 6A1

60 70 80 90 100
 GGTGACCCGCAAGGCCATGCGCACCCTCACCAACATCTTTATCTGCT
 CCACTGGGCGTCGTTCCGGTACCGGTGGCAGTGGTTGTAGAAATAGACGA
 V T R S K A M R T V T N I F I C>

TRANSLATION OF GA1.TXT [A]

6A F 32

110 120 130 140 150
 CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCATTCCCGTCACC
 GGAACCGCGAGTCACTGGACGAGTAGTGAAGAAGACGTAAGGGCAGTGG
 S L A L S D L L I T F F C I P V T>

TRANSLATION OF GA1.TXT [A]

to order
for labeling

3' Race

160
 ATGAAGCCGAA
 TACTTCGGCTT
 M K P X>

41 22 188 167 53.9 78.0 3.5 56.7 60.4 56.8 48.1 48.1 -3.6 -8.3

CCTTTGGCAATGCTCTGGTGTCTAC 27 -43.6 -199.5 -515.1⁺ CCATCTAATACGACTCACTATAGGC 27 -43.0 -205.0 -536.4

GA1-F41 (Brian Boockvar 1/9/05)

32 74 188 115 52.2 75.4 1.7 54.9 58.6 56.8 48.0 48.1 -4.4 -8.3

GCACCTCACCAACATCTTTATCTG 25 -40.2 -182.9 -471.0⁺

GA1-F32 (Brian Boockvar 1/9/05)

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CROSS REFERENCES.

BAYER CORPORATION

SUBJECT

Touch Down PCR for GAI RACE

15	5 μ l	cDNA template	(Heart)	(Brain)	1
08	36 μ l	H ₂ O			2
15	5 μ l	10 \times cDNA Buffer			3
3	1 μ l	2NTP Mix (10mM)			4
3	1 μ l	Ad6 cDNA prep mix (50 \times)			5
					6
	43 μ l	Final	+ 3 μ l	AD1	7

Program 1 (preferred; use if GSP T_m > 70°C):

PE DNA Thermal

PE GeneAmp Systems 2400/9600
(or hot-lid thermal cycler):

• 94°C for 30 sec

• 5 cycles:

94°C 5 sec

72°C 4 min°

• 5 cycles:

94°C 5 sec

70°C 4 min°

• 20–25 cycles:

94°C 5 sec

68°C 4 min°

Heart	1	B126
	2	F32
	3	F41
Brain	4	B126
	5	F32
	6	F41

PRODUCT: Human Heart
Marathon-Ready™ cDNA

CATALOG #: 7404-1

LOT#: 9010719

STORAGE BUFFER:

10 mM Tricine-KOH (pH 9.2)
1 mM EDTA

STORAGE CONDITIONS:

-20°C
Avoid multiple freeze/thaw cycles.

SHELF LIFE:

1 year from date of receipt under
proper storage conditions

DESCRIPTION:

Marathon-Ready cDNA is high-quality, double-stranded cDNA which has been ligated to the Marathon™ Adaptor and is ready for use as a template in 5' and 3' Marathon RACE reactions. In many cases, the full-length cDNA can then be obtained by end-to-end amplification or standard cloning. Enough material is provided for 30 50- μ l Marathon RACE reactions.

CONCENTRATION: \approx 0.1 ng/ μ lPOLY A⁺ RNA SOURCE:

Normal, whole hearts pooled from 3 male
Caucasians, ages 28–47; cause of death: trauma

No further RNA source information is available.

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DATE

Exhibit 13

3'-RACE #2 is assembled
from LZLZ11 and LZLZ21

BAYER CORPORATION

SUBJECT human GAL project. Full length 5' + 3' ends.

1 new sequence was deposited in the Life Tools
2 of unknown protein and called GAL. pep.

349 AA.

1047 b.p. Long

3' Race#2 clone (8.27)
Sequencher™ "gal 3' 5' "

5' GAL consensus	atg cag cgc att aac att acc cgc gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac cgg ctg cga cgc ctc gtc	1
	atg cag cgc att aac att acc cgc gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac cgg ctg cga cgc ctc gtc	2
	Q A L N I T P E Q F S R L L R D H N L T R E Q F I A L Y R L R P L V	3
5' GAL consensus #106	tac acc cca gag ctg cgc gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg ggc ctc ttt ggc aat gct ctg gtg ttc tac gtg gtg	4
	tac acc cca gag ctg cgc gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg ggc ctc ttt ggc aat gct ctg gtg ttc tac gtg gtg	5
	Y T P E L P G R A K L A L V L T G V L I F A L A L F G N A L V F Y V V	6
5' GAL consensus 45 JZ11 #211	acc cgc agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg cgc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg	7
	gc acg gtc acc aac atc ttt atc tgc tcc ttg cgc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag	8
	acc cgc agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg cgc ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag	9
	T R S K A M R T V T N I F I C S L A L S D L I T F F C I P V T M L Q	10
45 JZ11 46 JZ11 #316	aac att tcc gac aac tgg ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct	11
	aac att tcc gac aac tgg ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct	12
	N I S D N W L G G A F I C K M V P F V Q S T A V V T E I L T M T C I A	13
45 JZ11 46 JZ11 #421	gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa atg aag tgg caa tac acc aac cga agg gct ttc aca atg cta ggt gtg gtc tgg ctg gtg gca gtc atc	14
	gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa atg aag tgg caa tac acc aac cga agg gct ttc aca atg cta ggt gtg gtc tgg ctg gtg gca gtc atc	15
	V E R H Q G L V H P F K M K W Q Y T N R R A F T M L G V V W L V A V I	16
45 JZ11 46 JZ11 #526	gta gga tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct gtg cac	17
	gta gga tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct gtg cac	18
	V G S P M W H V Q Q L E I K Y D F L Y E K E H I C C L E E W T S P V H	19
45 JZ11 46 JZ11 #631	cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att ggt tat gaa ctt tgg ata aag aaa	20
	cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att ggt tat gaa ctt tgg ata aag aaa	21
	Q K I Y T T F I L V I L F L L P L M V M L I L Y S K I G Y E L W I K K	22
45 JZ11 46 JZ11 #736	aga gtt ggg gat ggt tca gtg ctt cga act att cat gga aaa gaa atg tcc aaa ata gcc agg aag aag aaa cga gct gtc att atg atg gtg aca gty gtg gct	23
	aga gtt ggg gat ggt tca gtg ctt cga act att cat gga aaa gaa atg tcc aaa ata gcc agg aag aag aaa cga gct gtc att atg atg gtg aca gty gtg gct	24
	aga gtt ggg gat ggt tca gtg ctt cga act att cat gga aaa gaa atg tcc aaa ata gcc agg aag aag aaa cga gct gtc att atg atg gtg aca gty gtg gct	25
	R V G D G S V L R T I H G K E M S K I A R K K K R A V I M M V T V V A	26
45 JZ11 46 JZ11 #841	ctc ttt gct gty tgc tgg gca cca ttc cat gtt gtc cat	27
	ctc ttt gct gty tgc tgg gca cca ttc cat gtt gtc cat atg atg att gaa tac agt aat ttt gaa aag gaa tat gat gat gtc aca atc aag atg att ttt gct	28
	ctc ttt gct gty tgc tgg gca cca ttc cat gtt gtc cat atg atg att gaa tac agt aat ttt gaa aag gaa tat gat gat gtc aca atc aag atg att ttt gct	29
	L F A V C W A P F H V V H M M I E Y S N P E K E Y D D V T I K M F	30
45 JZ11 46 JZ11 #841	atc gtg caa att att gga ttt tcc aac tcc atc tgt aat ccc att gtc tac gca ttt atg aat gaa aac ttc gaa aaa aaa aaa aaa aag ggc tgc tga att	31
	atc gtg caa att att gga ttt tcc aac tcc atc tgt aat ccc att gtc tac gca ttt atg aat gaa aac ttc gaa aaa aaa aaa aaa aag ggc tgc tga att	32
	I V Q I I G F S N S I C N P I V Y A F M N E N F E K K K K K S G R	33
45 JZ11 46 JZ11 #841	cta gac ctg ccc ggg cgg ccc gct cga gcc cta tag tga gta tgc gat ccc cgg gta cgc agc tgc aat tca ctg gcc gtc gtt tta caa ag	34
	cta gac ctg ccc ggg cgg ccc gct cga gcc cta tag tga gta tgc gat ccc cgg gta cgc agc tgc aat tca ctg gcc gtc gtt tta caa ag	35
	L D L P G R P A R A L V S D P R V P S S N S L A V V L Q	36

GAL - Back primer

poly A tail

Marathon 2.0

Primer

CGC GGT ATT TTA

1 2 3 4 5 6 7 8 9 Back

STOP

Exhibit 14

Alignment of 3'-RACE #2
with SEQ ID NO 1 and SEQ
ID NO 2

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75

76 ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC AAG CTG GCC CTC GTG CTC 150

151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG ACC CGC AGC AAG GCC 225

3'-RACE #2 5' -

1 GCG ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTT TGC ATT CCC 71
226 ATG CCG ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTT TGC ATT CCC 300

72 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTG CAG 146
301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTG CAG 375

147 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 221
376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450

222 TTT AAA ATG AAG TGG CAA TAC ACC AAC CAA AGG GCT TTC ACA ATG CTA GGT GTG TGG CTG GTG GCA GTG ATC 296
451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CAA AGG GCT TTC ACA ATG CTA GGT GTG TGG CTG GTG GCA GTG ATC 525

297 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 371
526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600

372 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTC CTG 446
601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTC CTG 675

447 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 521
676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750

522 TCA GTG CTT CGA ACT ATT CAT GGA AAA ATG TCC AAA ATA GCC AAG AAG AAA CGA GCT GTG ATT ATG ATG 596
751 TCA GTG CTT CGA ACT ATT CAT GGA AAA ATG TCC AAA ATA GCC AAG AAG AAA CGA GCT GTG ATT ATG ATG 825

597 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGG GCA CCA TTC CAT GTT GTG CAT ATG ATG ATT GAA TAC AGT AAT 671
826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGG GCA CCA TTC CAT GTT GTG CAT ATG ATG ATT GAA TAC AGT AAT 900

672 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 746
901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975

-3' 3'-RACE #2

747 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTGAAAAA
976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTGAAAAA

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200
1201 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275
1276 CCT TTA GAC AGT GGG CAT TAA 1296

1	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	L	R	D	H	N	L	T	R	E	Q	F		
26	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L		
51	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A		
76	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P		
100			T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P		
125			V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q
150			V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q
175			S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P
200			S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P
225			F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I
250			F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I
275			V	G	S	P	M	W	H	V	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	
300			V	G	S	P	M	W	H	V	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	
325			C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L
350			C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L
375			P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G
400			P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G
425			S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	K	R	A	V	I	M	M
450			S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	K	R	A	V	I	M	M
475			V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N
500			V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N
525			F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S
550			F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S
575			I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C
600			I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C
625			I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C
650			I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C
675			I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C

Exhibit 15

Alignment of virtual 1036
nucleotide clone with SEQ
ID NO 1 and SEQ ID NO 2

5GA1 5' - GGTGGCCCCGGTCCGGGAGCGCACAGCA

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CAG CAC AAC CTG ACG CGG GAG CAG TTC
ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CAG CAC AAC CTG ACG CGG GAG CAG TTC

75

76 ATC GCT CTG TAC CCG CTG CGA CCG CTG CTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC
ATC GCT CTG TAC CCG CTG CGA CCG CTG CTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC

150

151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC CTG GTG ACC CGC AGC AAG GCC
ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC CTG GTG ACC CGC AGC AAG GCC

225

226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC
ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC

300

— AAGCCGAA-3' 5GA1

L2L21 5' -

301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG
GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG

375

376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT
TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT

450

451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC
TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC

525

526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC
GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC

600

601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTG
TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTG

675

676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT
CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT

750

-3' LZLZ11

751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG

826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900
GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT

901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975
TTT GAA AAG GAA TAT GAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC

-3' LZLZ21

1036 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC GAAAAA
976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050

1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AAG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125

1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200

1201 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275

1276 CCT TTA GAC AGT GGG CAT TAA 1296

[illegible]

Exhibit 16

Names of IMAGE/Unigene
clones

BAYER CORPORATION

SUBJECT

Image Clones matching 6A1

m	2055532	g4001837	1
			2
m	2055185	g4002759	3
			4
			5
			6
m	2091776	g4187861	7

DNA vs EST Homology Search

source
g4001837
GB:g4001837
GB:g4002759
GB:g4187861

g4001837

Hit ID	P-Value	% ident.	Description
GB:g4001837 (Detail)	0	100	tb27a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

Is Analysis Results: 28499

http://lifetools-e.wh.bayer.com/cgi-bin/incyte/LifeTools/2.0/LT_View?id=28499

GB:g4002759 (Detail)	0	100	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

GB:g4187861 (Detail)	6.2e-43	100	te67e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens
Feature	Start	Stop	Description
source	3	127	

Acc. Num.	Image/Unigene TIGR Indices	Insert Length	Read Length	HQSS	Source (Age/Sex)
AI307658	Im:2055532 Hs.181638	1414	432	419	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI308124	Im:2055185 Hs.181638	1308	432	429	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI378008	Im:2091776 Hs.181638	404	364		Soares_NFL_T_GBC_S1 library made from pooled

		20
		27
2	(3,4)	28
		29
2	(1,2)	30
		31
		32
		33
3	5,6	34

EYNOLDS / NILES, MI * SEPT. 92

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

Exhibit 17

Location of in-frame STOP
codon in sequence upstream
of START methionine

NRV - Like Clow and primers -

LGZ1.seq -> Genes

DNA sequence 1902 b.p. TGGCCTCGAGG ... CTGTGTCCTTC linear

1 TGGCCCTTCGAGGCCCAAGAATTCCGACACGAGGAGCGGGGAGCCAGGAGCCGAGCAACCTTCGGTGGCGCTCCAGCACCACAGACCCGAGCGGCGCTCG 100

101 CCTTAGGGAAGAGCAAGGGAAGAACCTTTATTTTGAACCGCGAATCTTTTGGTCTACTGAGATCGAGTCTCCAGTGCCTTTGGCTTCCCGCTCTTTTATCG 200

201 TGGGTTTGATCCCTGAGCTGCTCTCTCTTCCCGAACCCTGCGGCTGTCAGCCTAGAGCCCTCCCGCGCGGCTGACTCCAGAGTAGAGGAGAGCGCGGCG 300

301 CTCGGCTGGTCCCGCGAAGCCCTCGCTGCCCCGCGAG ATG CGG ATG GCC AGC CAG TAG CGGGCGGTGGCCCCGCGCTGAGGAGAGCGAGC 392

1 M R M A S Q * 7

393 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CGG GAC CAC AAC CTG ACG CGG GAG CAG 465

1 L N I T P E Q F S R L L R D H N L T R E Q 24

466 TTC ATC GCT CTG TAC CGG CTG CGA CCG CTC GTC TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG 540

25 F I A L Y R L R P Y P E L P G R A L A L V 49

541 CTC ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GCG AAT GCT CTG GTG TTC TAG GTG GTG ACC CGC AGC AAG 615

50 L T G V L I F A L A L G N A L V F Y V V T R S K 74

616 GCC ATG GCG ACC GTC ACC AAC ATC TTT ATC TGT TTT GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT 690

75 A M R T V T N I F I C S A L S D L L I T F F C I 99

691 CCC GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG GCG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC 765

100 P V T M L Q N I S D N W L G G A F I C K M V P F V 124

766 CAG TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT 840

125 Q S T A V V T E I L T M T C I A V E R H Q G L V H 149

841 CCT TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC 915

150 P F K M C K W Y T N R R A F T M L G V V W L V A V 174

916 ATC GTA GGA TCA CCK ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC 990

175 I V G S P M W H V Q Q L E I K Y D F L Y E K E H I 199

991 TGC TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC 1065

200 C C L E E W T S P V H Q K I Y T T F I L V I L F L 224

1066 CTG CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT 1140

225 L P L M V M L I L Y S K I G Y E L W I K K R V G D 249

1141 GGT TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG 1215

250 G S V L R T I H G K E M S K I A R K K K R A V I 274

1216 ATG GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT 1290

275 M V T V V A L F A V C W A P F H V V H M M I E Y S 299

1291 AAT TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCG AAC 1365

300 N F E K E Y D V T I K M I F A I V Q I I G F S N 324

1366 TAT GCA TTT ATG AAT GAA AAC TTC AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT 1440

325 S I C N P I W Y A M N E N F K K N V L S A V C Y 349

1441 TGC ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA 1515

350 C I V N K T F S P A Q R H G N S G I T M M R K K A 374

1516 AAG TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA 1590

375 K F S L R E N P V E E T K G E A F S D G N I E V K 399

1591 TTG TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT 1665

400 L C E Q T E E K K K L K R H L A L F R S E L A E N 424

1666 TCT CCT TTA GAC AGT GGG CAT TAA TTAATAAATATCTTCATAATTA ATG CCC TTC AGA TTG TAA CCAAGGCAAAATATTTT 1750

425 S P L D S G H * M P F R L 6

1751 GAGCAAGGTCAAATACTCTTTTATCTCTTAAG ATG ATG ACA AGA AGA AAA CAA ATC ATG TTT CCA TTA AAA AAT GAC ACG 1831

1 M M T R R K Q I M F P L K N D T 16

1832 AGG CTA GTC CAA GTG CAG TGA TGT TAC AAT TATGATCACAATCATTTAACACATTTCTGTGTCCTTC 1902

17 R L V I O B 23

B 23

SIGNED BY

WITNESSED AND UNDERSTOOD BY

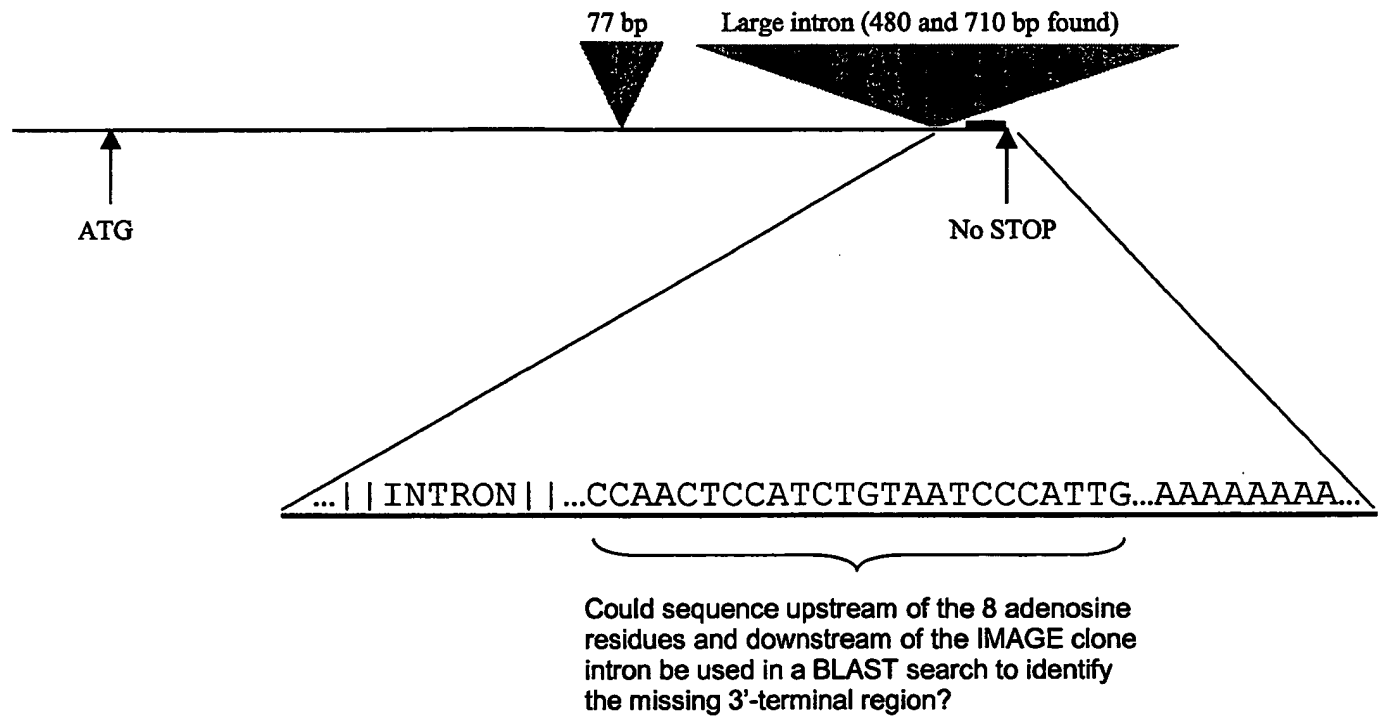
DATE

DATE _____

Exhibit 18

Cloning the 3'-end based on
IMAGE sequence clues and
genomic structure of our
novel GPCR

Diagram of IMAGE clone structure and BLAST search strategy



Preliminary genomic structure of novel GCPR

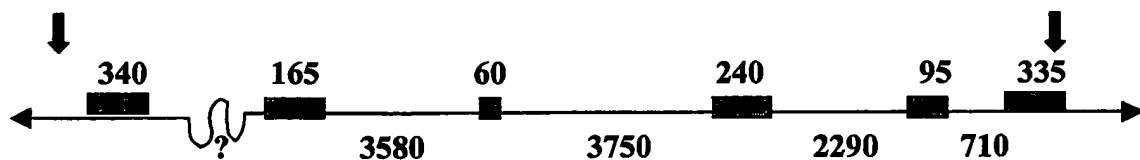


Exhibit 19

Final electronically
assembled novel GPCR
(named LGZ1)

BAYER CORPORATION

SUBJECT

NRV - Like clone and primers.

DNA Strider™ 1.2

LGZ1.seq -> Genes

DNA sequence 1902 b.p. TGGCCCTCGAGG ... CTGTGTTCCCTC linear

13
✓
10, 14, 15, 16

Notably
- Bloomquist 6/21/05

↓
C C A A 6 6

sty

CC TT 6/6

66 AAC

3			

C	C	T	A

2	2	7	6
6	6	7	6

6	6	A	A	C

a			e
		A	

CTA

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[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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12	5
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12	2	

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DS & REYNOLDS / N

SIGNED BY**DATE**

WITNESSED AND UNDERSTOOD BY

DATE _____

ADOLF DEERFLIANG.

Exhibit 20

Alignment of final 300 3'-
nucleotides against SEQ ID
NO 1

1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG GAC CAC AAC CTG ACG CGG GAG CAG TTC 75
76 ATC GCT CTG TAC CCG CTG CGA CCG CTC GTG TAC ACC CCA GAG CTG CCG GGA CGC GCC AAG CTG GCC CTC GTG CTC 150
151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG ACC CGC AGC AAG GCC 225
226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ACC TTC TTT TGC ATT CCC 300
301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375
376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450
451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GCA GTC ATC 525
526 GTA GGA TCA CCC ATG TGG CAC GTG CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600
601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTG ATC CTC TTC CTC CTG 675
676 CCT CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750
751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900
901 TTT GAA AAG GAA TAT GAT GAT GTC ACA ATC AAG ATG ATT TTT GCT ATC GTG CAA ATT ATT GGA TTT TCC AAC TCC 975
1
976 ATC TGT AAT CCC ATT GTC TAT GCA TTT ATG AAT GAA AAC TTC
AAA AAA AAT GTT TTG TCT TCT GCA GTT TGT TAT TGC 33
AAA AAA AAT GTT TTG TCT GCA GTT TGT TAT TGC 1050
34 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 108
1051 ATA GTA AAT AAA ACC TTC TCT CCA GCA CAA AGG CAT GGA AAT TCA GGA ATT ACA ATG ATG CGG AAG AAA GCA AAG 1125
109 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 183
1126 TTT TCC CTC AGA GAG AAT CCA GTG GAG GAA ACC AAA GGA GAA GAA GCA TTC AGT GAT GGC AAC ATT GAA GTC AAA TTG 1200
184 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 258
1201 TGT GAA CAG ACA GAG GAG AAG AAA AAG CTC AAA CGA CAT CTT GCT CTC TTT AGG TCT GAA CTG GCT GAG AAT TCT 1275
259 CCT TTA GAC AGT GGG CAT TAA
1276 CCT TTA GAC AGT GGG CAT TAA
TATAACAATATCTTCATAT 300
1296

Exhibit 21

Final cloned full-length novel
GPCR

BAYER CORPORATION

SUBJECT

Sequencing results of LGZ1/pT7Blue.

1. Check if I. Taylor going to clone p.6. receptor and when?

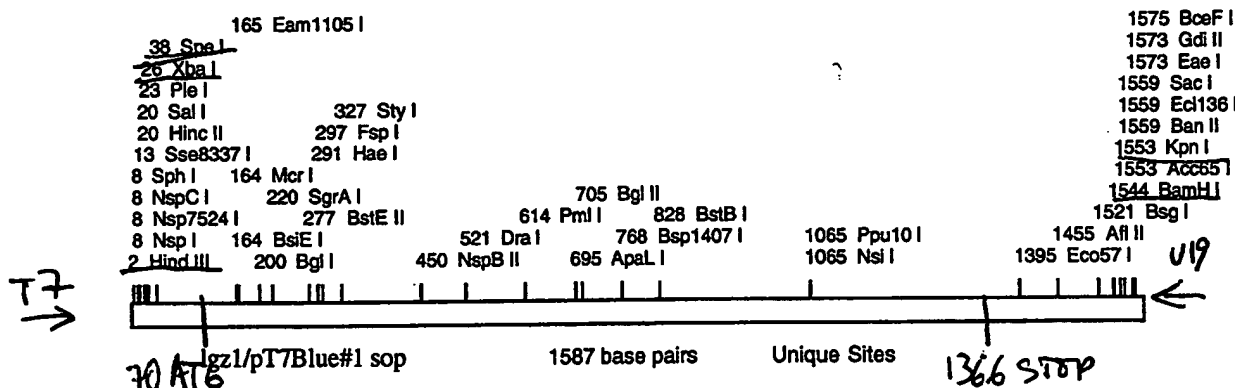
1). Clone #1 sop is ok with one polymorphic

DNA Strider™ 1.2

lgz1/pT7Blue#1 sop -> Graphic Map

DNA sequence 1587 b.p. caagcttgcattg ... ccgtcggtttaca linear

432 AA



2) Clone #7 H. Brain is good (same orientation) with: ttt → ttc (Phe) 417 AA

3) Clone #16 H. Heart is good with: atc → Att (Ile) 216 AA

↓ cloned using TA-kit in penta 3.1 His.

Xba/Bam 3.1 (-)
Kpn(II)

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

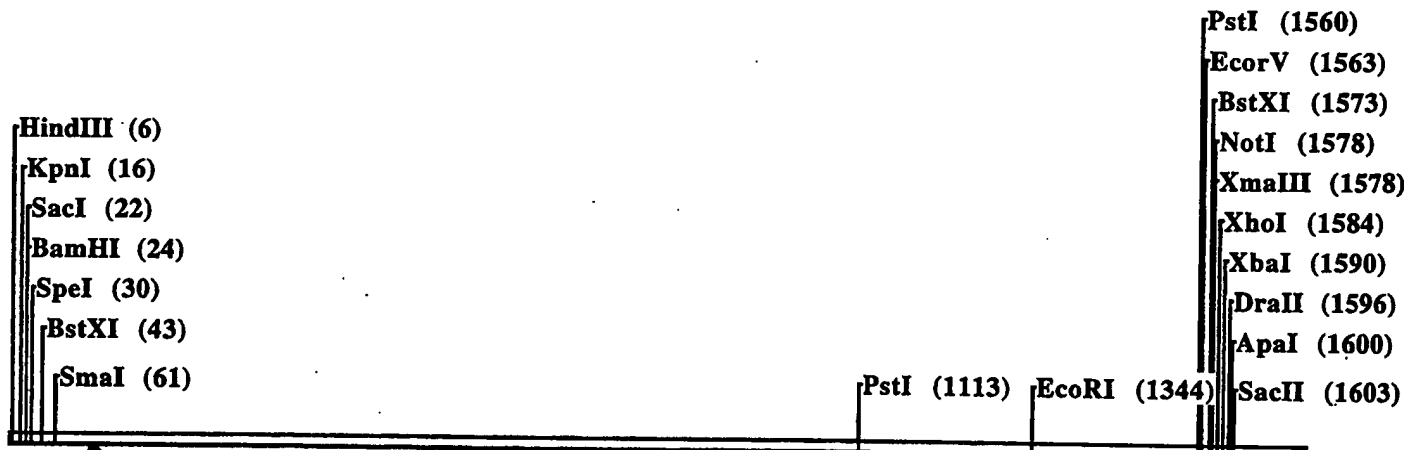
CROSS REFERENCES:

BAYER CORPORATION

SUBJECT

Full length cDNA of LGZ1 (NPY-like)

```
#1sop/pcDNA3.1Topo
Sequencher™ "Untitled Project"
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ATG (69)

Mapping all cutsites.

Cutters : Apal, BamHI, BstXI, DraII, EcoRI, EcorV, HindIII, KpnI, NotI, PstI, SacI, SacII, SmaI, SpeI, XbaI, XhoI & XmaII

Non-Cutters : Bsp106 & SalI

#Lsop/pdNA3.1Topo
Sequencher™ "Untitled Project"

PCR of LG21 fr. 02_12_21 #1

ctc cgg gag cgc aca gca atg cag gcg ctt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac cgg ctg cga cgg
tcc cgg gag cgc aca gca atg cag gcg ctt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac cgg ctg cga cgg

ctc cgg gag cgc aca gca atg cag gcg ctt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gac cac aac ctg acg cgg gag cag ttc atc gct ctg tac cgg ctg cga cgg
Ser Arg Glu Arg Thr Ala MET Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg Asp His Asn Leu Thr Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg Pro

PCR of LG21 fr. 02_12_21 #118

ctc gtc tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg gcg ctg ttt ggc aat gct ctg gtg ttc tac gtg gtg acc cgc
ctc gtc tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg gcg ctg ttt ggc aat gct ctg gtg ttc tac gtg gtg acc cgc

ctc gtc tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctc gtg ctc acc ggc gtg ctc atc ttc gcc ctg gcg ctg ttt ggc aat gct ctg gtg ttc tac gtg gtg acc cgc
Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala Leu Val Phe Tyr Val Val Thr Arg

PCR of LG21 fr. 02_12_21 03_12_22 #235

agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg
agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg
agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg

agc aag gcc atg cgc acc gtc acc aac atc ttt atc tgc tcc ttg gcg ctc agt gac ctg ctc atc acc ttc ttc tgc att ccc gtc acc atg ctc cag aac att tcc gac aac tgg
Ser Lys Ala MET Arg Thr Val Thr Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe Phe Cys Ile Pro Val Thr MET Leu Gln Asn Ile Ser Asp Asn Trp

PCR of LG21 fr. 02_12_21 03_12_22 #352

ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct
ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct
ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct

ctg ggg ggt gct ttc att tgc aag atg gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct
Leu Gly Gly Ala Phe Ile Cys Lys MET Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu Ile Leu Thr MET Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val His Pro

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES:

BAYER CORPORATION

SUBJECT

1MA.6E

[illegible]

CROSS REFERENCES:

Exhibit 22

Alignment of LGZ1 clone
DNA sequence with SEQ ID
NO 1

19 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CAC AAC CAC CTG ACG CGG GAG CAG TTC 93
1 ATG CAG GCG CTT AAC ATT ACC CCG GAG CAG TTC TCT CGG CTG CTG CAC AAC CAC CTG ACG CGG GAG CAG TTC 75
1 M Q A L N I T P E Q F S R L L L R D H N L T R E Q F 25

94 ATC GCT CTG TAC CCG CTG CGA CCG CTG CTC TAC ACC CCA GAG CTG CCG GGA CGC GGC AAG CTG GCC CTC CTG CTC 168
76 ATC GCT CTG TAC CCG CTG CGA CCG CTG CTC TAC ACC CCA GAG CTG CCG GGA CGC GGC AAG CTG GCC CTC CTG CTC 150
26 I A L Y R L R P L V Y T P E L P G R A K L A L V L 50

169 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG ACC CGC AGC AAG GCC 243
151 ACC GGC GTG CTC ATC TTC GCC CTG GCG CTC TTT GGC AAT GCT CTG GTG TTC TAC GTG ACC CGC AGC AAG GCC 225
51 T G V L I F A L A L F G N A L V F Y V T R S K A 75

244 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 318
226 ATG CGC ACC GTC ACC AAC ATC TTT ATC TGC TCC TTG GCG CTC AGT GAC CTG CTC ATC ACC TTC TTC TGC ATT CCC 300
76 M R T V T N I F I C S L A L S D L L I T F F C I P 100

319 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 393
301 GTC ACC ATG CTC CAG AAC ATT TCC GAC AAC TGG CTG GGG GGT GCT TTC ATT TGC AAG ATG GTG CCA TTT GTC CAG 375
101 V T M L Q N I S D N W L G G A F I C K M V P F V Q 125

394 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 468
376 TCT ACC GCT GTT GTG ACA GAA ATC CTC ACT ATG ACC TGC ATT GCT GTG GAA AGG CAC CAG GGA CTT GTG CAT CCT 450
126 S T A V V T E I L T M T C I A V E R H Q G L V H P 150

469 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 543
451 TTT AAA ATG AAG TGG CAA TAC ACC AAC CGA AGG GCT TTC ACA ATG CTA GGT GTG GTC TGG CTG GTG GCA GTC ATC 525
151 F K M K W Q Y T N R A F T M L G V V W L V A V I 175

544 GTA GGA TCA CCC ATG TGG CAC CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 618
526 GTA GGA TCA CCC ATG TGG CAC CAA CAA CTT GAG ATC AAA TAT GAC TTC CTA TAT GAA AAG GAA CAC ATC TGC 600
176 V G S P M W H V Q Q L E I K Y D F L Y E K E H I C 200

619 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC CTG 693
601 TGC TTA GAA GAG TGG ACC AGC CCT GTG CAC CAG AAG ATC TAC ACC ACC TTC ATC CTT GTC ATC CTC TTC CTC CTG 675
201 C L E E W T S P V H Q K I Y T T F I L V I L F L L 225

694 CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 768
676 CTT ATG GTG ATG CTT ATT CTG TAC AGT AAA ATT GGT TAT GAA CTT TGG ATA AAG AAA AGA GTT GGG GAT GGT 750
226 P L M V M L I L Y S K I G Y E L W I K K R V G D G 250

769 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 843
751 TCA GTG CTT CGA ACT ATT CAT GGA AAA GAA ATG TCC AAA ATA GCC AGG AAG AAG AAA CGA GCT GTC ATT ATG ATG 825
251 S V L R T I H G K E M S K I A R K K R A V I M M 275

844 GTC ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 918
826 GTG ACA GTG GTG GCT CTC TTT GCT GTG TGC TGG GCA CCA TTC CAT GTT GTC CAT ATG ATG ATT GAA TAC AGT AAT 900
276 V T V V A L F A V C W A P F H V V H M M I E Y S N 300

919	TTT	GAA	AAG	GAA	TAT	GAT	GAT	GTC	ACA	ATC	AAG	ATG	ATT	TTT	GCT	ATC	GTG	CAA	ATT	ATT	GGA	TTT	TCC	AAC	TCC	993	
901	TTT	GAA	AAG	GAA	TAT	GAT	GAT	GTC	ACA	ATC	AAG	ATG	ATT	TTT	GCT	ATC	GTG	CAA	ATT	ATT	GGA	TTT	TCC	AAC	TCC	975	
301	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	325	
994	ATC	TGT	AAT	CCC	ATT	GTC	TAT	GCA	TTT	ATG	AAT	GAA	AAC	TTC	AAA	AAA	AAT	GTT	TTG	TCT	GCA	GTT	TGT	TAT	TGC	1068	
976	ATC	TGT	AAT	CCC	ATT	GTC	TAT	GCA	TTT	ATG	AAT	GAA	AAC	TTC	AAA	AAA	AAT	GTT	TTG	TCT	GCA	GTT	TGT	TAT	TGC	1050	
326	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C	350	
1069	ATA	GTA	AAT	AAA	ACC	TTC	TCT	CCA	GCA	CAA	AGG	CAT	GGA	AAT	TCA	GGA	ATT	ACA	ATG	ATG	ATG	CGG	AAG	AAA	GCA	AAG	1143
1051	ATA	GTA	AAT	AAA	ACC	TTC	TCT	CCA	GCA	CAA	AGG	CAT	GGA	AAT	TCA	GGA	ATT	ACA	ATG	ATG	ATG	CGG	AAG	AAA	GCA	AAG	1125
351	I	V	N	K	T	F	S	P	A	Q	R	H	G	N	S	G	I	T	M	M	R	K	K	A	K	375	
1144	TTT	TCC	CTC	AGA	GAG	AAT	CCA	GTG	GAG	GAA	ACC	AAA	GGA	GAA	GCA	TTC	AGT	GAT	GGC	AAC	ATT	GAA	GTC	AAA	TTG	1218	
1126	TTT	TCC	CTC	AGA	GAG	AAT	CCA	GTG	GAG	GAA	ACC	AAA	GGA	GAA	GCA	TTC	AGT	GAT	GGC	AAC	ATT	GAA	GTC	AAA	TTG	1200	
376	F	S	L	R	E	N	P	V	E	E	T	K	G	E	A	F	S	D	G	N	I	E	V	K	L	400	
1219	TGT	GAA	CAG	ACA	GAG	GAG	AAG	AAA	AAG	CTC	AAA	CGA	CAT	CTT	GCT	CTC	TTT	AGG	TCT	GAA	CTG	GCT	GAG	AAT	TCT	1293	
1201	TGT	GAA	CAG	ACA	GAG	GAG	AAG	AAA	AAG	CTC	AAA	CGA	CAT	CTT	GCT	CTC	TTT	AGG	TCT	GAA	CTG	GCT	GAG	AAT	TCT	1275	
401	C	E	Q	T	E	E	K	K	L	K	R	H	L	A	L	F	R	S	E	L	A	E	N	S	425		
1294	CCT	TTA	GAC	AGT	GGG	CAT	TAA	TTATAACAATATCTTCATAAT																1335			
1276	CCT	TTA	GAC	AGT	GGG	CAT	TAA																	1296			
426	P	L	D	S	G	H	*																	431			

Exhibit 23

Alignment of LGZ1 clone
amino acid sequence with
SEQ ID NO 2

1	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	L	R	D	H	N	L	T	R	E	Q	F	25
	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	L	R	D	H	N	L	T	R	E	Q	F	
26	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	50
	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	
51	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	75
	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	
76	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P	100
	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P	
101	V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	125
	V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	
126	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	150
	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	
151	F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	175
	F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	
176	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	200
	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	
201	C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	225
	C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	
226	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	250
	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	
251	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M	275	
	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	R	A	V	I	M	M		
276	V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	300
	V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	
301	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	325
	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	
326	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C	350
	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C	
351	I	V	N	K	T	F	S	P	A	Q	R	H														

Exhibit 24

Alignment of assembled
fragments composing LGZ1
with SEQ ID NO 2

5GA1

1	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	L	R	D	H	N	L	T	R	E	Q	F	25
	M	Q	A	L	N	I	T	P	E	Q	F	S	R	L	L	R	D	H	N	L	T	R	E	Q	F	
26	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	50
	I	A	L	Y	R	L	R	P	L	V	Y	T	P	E	L	P	G	R	A	K	L	A	L	V	L	
51	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	75
	T	G	V	L	I	F	A	L	A	L	F	G	N	A	L	V	F	Y	V	V	T	R	S	K	A	
76	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P	100
	M	R	T	V	T	N	I	F	I	C	S	L	A	L	S	D	L	L	I	T	F	F	C	I	P	
101	V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	125
	V	T	M	L	Q	N	I	S	D	N	W	L	G	G	A	F	I	C	K	M	V	P	F	V	Q	
126	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	150
	S	T	A	V	V	T	E	I	L	T	M	T	C	I	A	V	E	R	H	Q	G	L	V	H	P	
151	F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	175
	F	K	M	K	W	Q	Y	T	N	R	R	A	F	T	M	L	G	V	V	W	L	V	A	V	I	
176	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	200
	V	G	S	P	M	W	H	V	Q	Q	L	E	I	K	Y	D	F	L	Y	E	K	E	H	I	C	
201	C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	225
	C	L	E	E	W	T	S	P	V	H	Q	K	I	Y	T	T	F	I	L	V	I	L	F	L	L	
226	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	250
	P	L	M	V	M	L	I	L	Y	S	K	I	G	Y	E	L	W	I	K	K	R	V	G	D	G	
251	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	K	R	A	V	I	M	M	275
	S	V	L	R	T	I	H	G	K	E	M	S	K	I	A	R	K	K	K	R	A	V	I	M	M	
276	V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	300
	V	T	V	V	A	L	F	A	V	C	W	A	P	F	H	V	V	H	M	M	I	E	Y	S	N	
301	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	325
	F	E	K	E	Y	D	D	V	T	I	K	M	I	F	A	I	V	Q	I	I	G	F	S	N	S	
326	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C	350
	I	C	N	P	I	V	Y	A	F	M	N	E	N	F	K	K	N	V	L	S	A	V	C	Y	C	

3'RACE #2

300 nt 3'-end

351 I V N K T F S P A Q R H G N S G I T M M R K K A K 375
I V N K T F S P A Q R H G N S G I T M M R K K A K

376 F S L R E N P V E E T K G E A F S D G N I E V K L 400
F S L R E N P V E E T K G E A F S D G N I E V K L

401 C E Q T E E K K K L K R H L A L F R S E L A E N S 425
C E Q T E E K K K L K R H L A L F R S E L A E N S

426 P L D S G H * 431
P L D S G H *

300 nt 3'-end

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